

SEQUENCE LISTING

<110> Croteau, Rodney B
Bohlmann, Joerg
Steele, Christopher L
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545

<151> 1999-07-26

<150> 60/052,249

<151> 1997-07-11

<150> PCT/US98/14528

<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

<210> 1

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<222> (69)..(1952)

<223> Clone AG2.2 encoding myrcene synthase

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Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
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ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
15 20 25 30

aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
35 40 45

cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
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caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
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Ala	Glu	Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	
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ctg	gat	gat	gga	aga	tta	atg	agt	tcc	ttt	aat	gat	ctc	atg	caa	cgc	446
Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
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ctt	tgg	ata	gtc	gat	agc	ggt	gaa	cgt	ttg	ggg	ata	gct	aga	cat	ttc	494
Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
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Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
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Glu	Asn	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	
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Ser	Thr	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	
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Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
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Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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Pro	Val	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	
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Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	
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Gln	Lys	Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	

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gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly 355 360 365			1166
ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp 370 375 380			1214
act ttt gga acg att gac gag ctt gaa ctc ttc aca tct gca att aag Thr Phe Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys 385 390 395			1262
aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys 400 405 410			1310
gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala 415 420 425 430			1358
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tgg ctt cct gat tac atc ttg aag gga att gat ttt cca tcc agg ttc Trp Leu Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe 495 500 505 510			1598
aat gat ttg gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys 515 520 525			1646
tac aag gcc gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys 530 535 540			1694
tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His 545 550 555			1742
atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu 560 565 570			1790

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 Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe
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agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt 1934
 Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
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gaa tct atg ctt ttt taa ctataacccat atccataata ataagctcat 1982
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<213> Abies grandis

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 35 40 45

Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
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Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
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Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
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Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
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Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
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Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
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Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
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Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	Glu	Ala	
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Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
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Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
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Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
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20 25 30

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Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro
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tcc atc agc atg agc tct acc acc gtt gta acc gat gat ggt gta cga 194
Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg
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aga cgc atg ggc gat ttc cat tcc aac ctc tgg gac gat gat gtc ata 242
Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile
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Glu Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu	
100 105 110	
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Glu Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu	
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Trp Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys	
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Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu	
145 150 155	
 aat ggc atc gga tgc ggg agg gag agt gtt gtt act gat ctg aac tca	530
Asn Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser	
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Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser	
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 tct gaa aat att cag aca gat gaa gag atc aga ggc gtt ctg aat tta	674
Ser Glu Asn Ile Gln Thr Asp Glu Glu Ile Arg Gly Val Leu Asn Leu	
210 215 220	
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Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Ile Met Asp Glu	
225 230 235	
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Ala Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile	
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Pro Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly	
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Trp His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val	
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Phe Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys	
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Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Gln Ser Leu Gln	
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Lys Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe	
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Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu	
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gct tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc	1106
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Glu Glu Ala Gln Gly Arg Asp Thr Leu Thr Tyr Ala Arg Glu Ala Trp	
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Glu Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr	
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Gly Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser	
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Cys Gly His Arg Ile Ser Ala Leu Gln Pro Ile Leu Thr Met Asp Ile	
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Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu	
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Asn Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys	
515 520 525	
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Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys	
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Tyr Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His	
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atc aac gcc atg atc agt gac gta atc aaa gga tta aat tgg gaa ctt	1730

Ile Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu
560 565 570 575

ctc aaa cca gac atc aat gtt ccc atc tcg gcg aag aaa cat gct ttt 1778
Leu Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe
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Asp Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr
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50 55 60

Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln
65 70 75 80

Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu
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Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu
100 105 110

Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp
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Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys Asp
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Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu Asn
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Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser Thr

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Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Ile	Met	Asp	Glu	Ala
225					230					235					240
Glu	Ile	Phe	Ser	Thr	Lys	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro
				245					250					255	
Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Gly	Asp	Val	Leu	Glu	Tyr	Gly	Trp
			260						265				270		
His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	Phe
		275					280					285			
Gly	Gln	Asp	Thr	Glu	Asn	Thr	Lys	Ser	Tyr	Val	Lys	Ser	Lys	Lys	Leu
	290					295					300				
Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Gln	Ser	Leu	Gln	Lys
305					310					315					320
Arg	Glu	Leu	Glu	Ser	Leu	Val	Arg	Trp	Trp	Lys	Glu	Ser	Gly	Phe	Pro
				325					330					335	
Glu	Met	Thr	Phe	Cys	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr	Leu	Ala
			340						345				350		
Ser	Cys	Ile	Ala	Phe	Glu	Pro	Gln	His	Ser	Gly	Phe	Arg	Leu	Gly	Phe
		355					360					365			
Ala	Lys	Thr	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	Thr
	370					375					380				
Phe	Gly	Thr	Val	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Thr	Met	Lys	Arg
385					390					395					400
Trp	Asp	Pro	Ser	Ser	Ile	Asp	Cys	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val
				405					410					415	
Tyr	Ile	Ala	Val	Tyr	Asp	Thr	Val	Asn	Glu	Met	Ala	Arg	Glu	Ala	Glu
			420						425				430		
Glu	Ala	Gln	Gly	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Arg	Glu	Ala	Trp	Glu
		435					440					445			
Ala	Tyr	Ile	Asp	Ser	Tyr	Met	Gln	Glu	Ala	Arg	Trp	Ile	Ala	Thr	Gly
	450					455				460					
Tyr	Leu	Pro	Ser	Phe	Asp	Glu	Tyr	Tyr	Glu	Asn	Gly	Lys	Val	Ser	Cys
465					470					475					480
Gly	His	Arg	Ile	Ser	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp	Ile	Pro
				485					490					495	

Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
500 505 510

Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
515 520 525

Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
530 535 540

Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
565 570 575

Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr Ser
595 600 605

Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu Glu
610 615 620

Ser Val Pro Leu
625

<210> 5
<211> 2089
<212> DNA
<213> Abies grandis

<220>
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<222> (73)..(1986)
<223> Clone AG10 encoding limonene synthase

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aggcaggaat cc atg gct ctc ctt tct atc gta tct ttg cag gtt ccc aaa 111
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys
1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303
Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
65 70 75

aac	ctg	tgg	gaa	gat	gat	ttc	ata	caa	tca	ttg	tcc	tca	cct	tat	ggg	351
Asn	Leu	Trp	Glu	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ser	Ser	Pro	Tyr	Gly	
	80						85					90				
gga	tct	tcg	tac	agt	gaa	cgt	gct	gag	aca	gtc	ggt	gag	gaa	gta	aaa	399
Gly	Ser	Ser	Tyr	Ser	Glu	Arg	Ala	Glu	Thr	Val	Val	Glu	Glu	Val	Lys	
	95					100					105					
gag	atg	ttc	aat	tca	ata	cca	aat	aat	aga	gaa	tta	ttt	ggt	tcc	caa	447
Glu	Met	Phe	Asn	Ser	Ile	Pro	Asn	Asn	Arg	Glu	Leu	Phe	Gly	Ser	Gln	
110					115					120					125	
aat	gat	ctc	ctt	aca	cgc	ctt	tgg	atg	gtg	gat	agc	att	gaa	cgt	ctg	495
Asn	Asp	Leu	Leu	Thr	Arg	Leu	Trp	Met	Val	Asp	Ser	Ile	Glu	Arg	Leu	
				130					135					140		
ggg	ata	gat	aga	cat	ttc	caa	aat	gag	ata	aga	gta	gcc	ctc	gat	tat	543
Gly	Ile	Asp	Arg	His	Phe	Gln	Asn	Glu	Ile	Arg	Val	Ala	Leu	Asp	Tyr	
			145					150					155			
ggt	tac	agt	tat	tgg	aag	gaa	aag	gaa	ggc	att	ggg	tgt	ggc	aga	gat	591
Val	Tyr	Ser	Tyr	Trp	Lys	Glu	Lys	Glu	Gly	Ile	Gly	Cys	Gly	Arg	Asp	
	160						165					170				
tct	act	ttt	cct	gat	ctc	aac	tcg	act	gcc	ttg	gcg	ctt	cga	act	ctt	639
Ser	Thr	Phe	Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	
	175					180					185					
cga	ctg	cac	gga	tac	aat	gtg	tct	tca	gat	gtg	ctg	gaa	tac	ttc	aaa	687
Arg	Leu	His	Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Glu	Tyr	Phe	Lys	
190					195					200					205	
gat	gaa	aag	ggg	cat	ttt	gcc	tgc	cct	gca	atc	cta	acc	gag	gga	cag	735
Asp	Glu	Lys	Gly	His	Phe	Ala	Cys	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Gln	
				210				215						220		
atc	act	aga	agt	gtt	cta	aat	tta	tat	cgg	gct	tcc	ctg	gtc	gcc	ttt	783
Ile	Thr	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Leu	Val	Ala	Phe	
			225					230					235			
ccc	ggg	gag	aaa	gtt	atg	gaa	gag	gct	gaa	atc	ttc	tcg	gca	tct	tat	831
Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ala	Ser	Tyr	
	240						245					250				
ttg	aaa	aaa	gtc	tta	caa	aag	att	ccg	gtc	tcc	aat	ctt	tca	gga	gag	879
Leu	Lys	Lys	Val	Leu	Gln	Lys	Ile	Pro	Val	Ser	Asn	Leu	Ser	Gly	Glu	
	255					260					265					
ata	gaa	tat	gtt	ttg	gaa	tat	ggt	tgg	cac	acg	aat	ttg	ccg	aga	ttg	927
Ile	Glu	Tyr	Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	
270					275					280					285	
gaa	gca	aga	aat	tat	atc	gag	gtc	tac	gag	cag	agc	ggc	tat	gaa	agc	975
Glu	Ala	Arg	Asn	Tyr	Ile	Glu	Val	Tyr	Glu	Gln	Ser	Gly	Tyr	Glu	Ser	
				290				295						300		
tta	aac	gag	atg	cca	tat	atg	aac	atg	aag	aag	ctt	tta	caa	ctt	gca	1023
Leu	Asn	Glu	Met	Pro	Tyr	Met	Asn	Met	Lys	Lys	Leu	Leu	Gln	Leu	Ala	
			305					310					315			

aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa	1071
Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln	
320 325 330	
tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt	1119
Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe	
335 340 345	
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct	1167
Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser	
350 355 360 365	
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt	1215
Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys	
370 375 380	
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg	1263
His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met	
385 390 395	
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca	1311
Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser	
400 405 410	
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg	1359
Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu	
415 420 425	
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc	1407
Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly	
430 435 440 445	
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat	1455
Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp	
450 455 460	
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg	1503
Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr	
465 470 475	
ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata	1551
Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile	
480 485 490	
gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac	1599
Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr	
495 500 505	
ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg	1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser	
510 515 520 525	
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg	1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg	
530 535 540	
gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat	1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His	
545 550 555	
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791

Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

taa aaacatatag aatgcattaa aatgtgggaa gtctataatc tagactattc 2036

tctatctttc ataatgtaga tctggatgtg tattgaactc taaaaaaaaa aaa 2089

<210> 6
<211> 637
<212> PRT
<213> Abies grandis

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20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr	Trp	Lys	Glu	Lys	Glu	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Thr	Phe	
				165					170					175		
Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	Arg	Leu	His	
			180					185					190			
Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Glu	Tyr	Phe	Lys	Asp	Glu	Lys	
		195					200					205				
Gly	His	Phe	Ala	Cys	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Gln	Ile	Thr	Arg	
	210					215					220					
Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu	
225					230					235					240	
Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Lys	
				245				250						255		
Val	Leu	Gln	Lys	Ile	Pro	Val	Ser	Asn	Leu	Ser	Gly	Glu	Ile	Glu	Tyr	
			260					265					270			
Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	
		275					280					285				
Asn	Tyr	Ile	Glu	Val	Tyr	Glu	Gln	Ser	Gly	Tyr	Glu	Ser	Leu	Asn	Glu	
	290					295					300					
Met	Pro	Tyr	Met	Asn	Met	Lys	Lys	Leu	Leu	Gln	Leu	Ala	Lys	Leu	Glu	
305					310					315					320	
Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Leu	Arg	Glu	Leu	Gln	Ser	Ile	Ser	
				325					330					335		
Arg	Trp	Trp	Lys	Glu	Ser	Gly	Ser	Ser	Gln	Leu	Thr	Phe	Thr	Arg	His	
			340					345					350			
Arg	His	Val	Glu	Tyr	Tyr	Thr	Met	Ala	Ser	Cys	Ile	Ser	Met	Leu	Pro	
		355					360					365				
Lys	His	Ser	Ala	Phe	Arg	Met	Glu	Phe	Val	Lys	Val	Cys	His	Leu	Val	
	370					375					380					
Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly	Thr	Met	Asn	Glu	Leu	
385					390					395					400	
Gln	Leu	Phe	Thr	Asp	Ala	Ile	Lys	Arg	Trp	Asp	Leu	Ser	Thr	Thr	Arg	
				405					410					415		
Trp	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys	
			420					425					430			
Ile	Asn	Glu	Met	Val	Glu	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Met	
		435					440					445				
Leu	Asn	Tyr	Ile	Gln	Asn	Ala	Trp	Glu	Ala	Leu	Phe	Asp	Thr	Phe	Met	
	450					455					460					
Gln	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Ser	Tyr	Leu	Pro	Thr	Phe	Glu	Glu	
465					470					475					480	
Tyr	Leu	Lys	Asn	Ala	Lys	Val	Ser	Ser	Gly	Ser	Arg	Ile	Ala	Thr	Leu	

485								490								495							
Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asp	Tyr	Ile	Leu	Gln								
			500								505				510								
Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Glu	Leu	Ala	Ser	Ser	Ile	Leu								
		515					520					525											
Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly								
	530					535					540												
Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	Pro	Gly	Ser								
545					550				555						560								
Ile	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn	Ala	Met	Ile	Ser	Asp	Ala								
			565						570					575									
Ile	Arg	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Pro	Asp	Ser	Lys	Ser	Pro								
		580					585						590										
Ile	Ser	Ser	Lys	Lys	His	Ala	Phe	Asp	Ile	Thr	Arg	Ala	Phe	His	His								
		595				600						605											
Val	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr	Thr	Val	Ser	Asn	Asn	Glu	Thr	Lys								
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625					630					635													

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Degenerate
 oligonucleotide PCR primer A wherein the letter
 "n" indicates an inosine residue

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> Degenerate oligonucleotide Primer A wherein n
 represents inosine

<400> 7
 arraygarra nggnrartay aarga

25

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: degenerate
 oligonucleotide PCR primer B wherein the letter
 "n" represents an inosine residue

<220>

<221> misc_feature
 <222> (1)..(20)
 <223> oligonucleotide PCR primer B wherein the letter n
 represents an inosine residue

<400> 8
 atgytnrcary tntaygargc

20

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: degenerate
 oligonucleotide PCR primer C wherein the letter
 "n" represents an inosine residue

<220>
 <221> misc_feature
 <222> (1)..(24)
 <223> PCR primer C wherein the letter n represents
 inosine

<400> 9
 ctnkynrang gnctratrta ckty

24

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: degenerate
 oligonucleotide PCR primer D wherein the letter
 "n" represents an inosine residue

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> PCR primer D wherein the letter n represents
 inosine

<400> 10
 gaygaynnnt wygaygcnya ygg

23

<210> 11
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<400> 11
 gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
 agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa 108

<210> 12

<211> 104
<212> DNA
<213> Abies grandis

<400> 12
gacgacgggt atgatgcgca tggaacgatt gacgagcttg aactcttcac atctgcaatt 60
aagagatgga attcatcaga gatagacagc ttccccgact atat 104

<210> 13
<211> 105
<212> DNA
<213> Abies grandis

<220>
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<222> (89)
<223> nucleotide may be a or c or g or t

<400> 13
gatgatgggt atgatgcgta cggaacgttg gaagaaatca aaatcatgac agagggagtg 60
agacgatggg atctttcggt gaccgcttnc cccgactata tgaaa 105

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<212> DNA
<213> Abies grandis

<220>
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<222> (93)
<223> nucleotide may be a or c or g or t

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agacgatggg atgtttcggt ggtagaccac ttnccccgac tacatgcaat ctagacc 117

<210> 15
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<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (2)..(2350)
<223> Clone AG1.28

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g ggt tat gat ctt gtg cat tct ctt aaa tca cct tat att gat tct agt 49
Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser
1 5 10 15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97
Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

aat	cca	gct	att	aca	gga	gat	gga	gaa	tca	atg	att	act	cca	tct	gct	145
Asn	Pro	Ala	Ile	Thr	Gly	Asp	Gly	Glu	Ser	Met	Ile	Thr	Pro	Ser	Ala	
		35					40					45				
tat	gac	aca	gca	tgg	gta	gcg	agg	gtg	ccc	gcc	att	gat	ggc	tct	gct	193
Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Val	Pro	Ala	Ile	Asp	Gly	Ser	Ala	
	50					55					60					
cgc	ccg	caa	ttt	ccc	caa	aca	gtt	gac	tgg	att	ttg	aaa	aac	cag	tta	241
Arg	Pro	Gln	Phe	Pro	Gln	Thr	Val	Asp	Trp	Ile	Leu	Lys	Asn	Gln	Leu	
	65				70					75					80	
aaa	gat	ggt	tca	tgg	gga	att	cag	tcc	cac	ttt	ctg	ctg	tcc	gac	cgt	289
Lys	Asp	Gly	Ser	Trp	Gly	Ile	Gln	Ser	His	Phe	Leu	Leu	Ser	Asp	Arg	
				85					90					95		
ctt	ctt	gcc	act	ctt	tct	tgt	gtt	ctt	gtg	ctc	ctt	aaa	tgg	aac	gtt	337
Leu	Leu	Ala	Thr	Leu	Ser	Cys	Val	Leu	Val	Leu	Leu	Lys	Trp	Asn	Val	
			100					105					110			
ggg	gat	ctg	caa	gta	gag	cag	gga	att	gaa	ttc	ata	aag	agc	aat	ctg	385
Gly	Asp	Leu	Gln	Val	Glu	Gln	Gly	Ile	Glu	Phe	Ile	Lys	Ser	Asn	Leu	
		115					120					125				
gaa	cta	gta	aag	gat	gaa	acc	gat	caa	gat	agc	ttg	gta	aca	gac	ttt	433
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Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Arg	Glu	Glu	Ile	Tyr	Ala	Val	Pro	
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Leu	Glu	Phe	Leu	Asn	Ser	Val	Met	Ile	Lys	Phe	Gly	Asn	Phe	Val	Pro	
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Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn	
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Pro	Leu	Glu	Phe	Tyr	Phe	Leu	Val	Ala	Ala	Gly	Thr	Tyr	Glu	Pro	Gln		
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Tyr	Ala	Lys	Cys	Arg	Phe	Leu	Phe	Thr	Lys	Val	Ala	Cys	Leu	Gln	Thr		

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 Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
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 Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
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 Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
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 Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
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 Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
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 Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
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 Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
 180 185 190
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 Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
 210 215 220
 Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
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Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His	
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Ser	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe		
			355					360					365				
ttc	ttc	aat	aca	gtg	aat	gaa	ttg	ata	gtt	gaa	atc	gtg	aaa	cgg	caa	1151	
Phe	Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln		
		370					375					380					
ggg	cgg	gat	atg	aca	acc	ata	gtt	aaa	gat	tgc	tgg	aag	cga	tac	att	1199	
Gly	Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile		
	385					390					395						
gag	tct	tat	ctg	caa	gaa	gcg	gaa	tgg	ata	gca	act	gga	cat	att	ccc	1247	
Glu	Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro		
400					405					410					415		
act	ttt	aac	gaa	tac	ata	aag	aac	ggc	atg	gct	agc	tca	ggg	atg	tgt	1295	
Thr	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys		
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att	gta	aat	ttg	aat	cca	ctt	ctc	ttg	ttg	ggt	aaa	ctt	ctc	ccc	gac	1343	
Ile	Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp		
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aac	att	ctg	gag	caa	ata	cat	tct	cca	tcc	aag	atc	ctg	gac	ctc	tta	1391	
Asn	Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu		
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gaa	ttg	acg	ggc	aga	atc	gcc	gat	gac	tta	aaa	gat	ttc	gag	gac	gag	1439	
Glu	Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu		
	465					470					475						
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Lys	Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln	Cys	Tyr	Met	Lys	Glu		
	480				485					490					495		
aat	cct	gaa	tct	aca	gtg	gaa	aat	gct	tta	aat	cac	ata	aaa	ggc	atc	1535	
Asn	Pro	Glu	Ser	Thr	Val	Glu	Asn	Ala	Leu	Asn	His	Ile	Lys	Gly	Ile		
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ctt	aat	cgt	tcc	ctt	gag	gaa	ttt	aat	tgg	gag	ttt	atg	aag	cag	gat	1583	
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Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly			
530	535	540	
ctt caa ttc atc tac aaa tac aga gac ggc tta tac att tct gac aag			1679
Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys			
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gaa gta aag gac cag ata ttc aaa att cta gtc cac caa gtt cca atg			1727
Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met			
560	565	570	575
gag gaa tag tgatgggtctt gggtttagtgt gtctattatg gtatatgtgca			1776
Glu Glu			
ttgacatttta tgcttaaagg tgtttcttaa acgttttaggg cggaccgtta aataagttgg			1836
caataattaa tatttagaga ctttgtggaa gtgttttaggg cataaaattg cctatggcct			1896
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Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His Leu			
35	40	45	
Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys			
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Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His			
65	70	75	80
Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp			
85	90	95	
Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys			
100	105	110	
Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg			
115	120	125	
Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly			
130	135	140	
Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln			
145	150	155	160

Val	Arg	Ser	Met	Leu	Ser	Leu	Leu	Arg	Ala	Ser	Glu	Ile	Ser	Phe	Pro	
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Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Arg	Glu	Tyr	Leu	
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Val	Pro	Arg	Trp	Glu	Ala	Arg	Ser	Phe	Leu	Glu	Ile	Tyr	Gly	His	Asn	
225				230						235					240	
His	Ser	Trp	Leu	Lys	Ser	Asn	Ile	Asn	Gln	Lys	Met	Leu	Lys	Leu	Ala	
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Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Lys	His	His	Lys	Glu	Ile	Gln	
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Phe	Ile	Thr	Arg	Trp	Trp	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Leu	Asn	Phe	
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Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys	Ile	
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Phe	Glu	Pro	Glu	Phe	Ser	Glu	Ser	Arg	Ile	Ala	Phe	Ala	Lys	Thr	Ala	
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Ile	Leu	Cys	Thr	Val	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Ala	Thr	Leu	
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His	Glu	Ile	Lys	Ile	Met	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Leu	Ser	
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Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe	Phe	
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Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln	Gly	
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Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile	Glu	
385					390					395					400	
Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro	Thr	
			405						410					415		
Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	Ile	
		420					425						430			
Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp	Asn	
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Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu	Glu	
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Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu	Lys	
465					470					475					480	

Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln	Cys	Tyr	Met	Lys	Glu	Asn
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Pro	Glu	Ser	Thr	Val	Glu	Asn	Ala	Leu	Asn	His	Ile	Lys	Gly	Ile	Leu
			500					505					510		
Asn	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Trp	Glu	Phe	Met	Lys	Gln	Asp	Ser
		515					520					525			
Val	Pro	Met	Cys	Cys	Lys	Lys	Phe	Thr	Phe	Asn	Ile	Gly	Arg	Gly	Leu
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Gln	Phe	Ile	Tyr	Lys	Tyr	Arg	Asp	Gly	Leu	Tyr	Ile	Ser	Asp	Lys	Glu
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Val	Lys	Asp	Gln	Ile	Phe	Lys	Ile	Leu	Val	His	Gln	Val	Pro	Met	Glu
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	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Thr	Asn	Tyr	Leu	Lys	
	1				5				10					15		
aaa	gtt	tta	gca	gga	cgg	gag	gct	acc	cac	gtc	gat	gaa	agc	ctt	ttg	95
Lys	Val	Leu	Ala	Gly	Arg	Glu	Ala	Thr	His	Val	Asp	Glu	Ser	Leu	Leu	
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gga	gag	gtg	aag	tac	gca	ttg	gag	ttt	cca	tgg	cat	tgc	agt	gtg	cag	143
Gly	Glu	Val	Lys	Tyr	Ala	Leu	Glu	Phe	Pro	Trp	His	Cys	Ser	Val	Gln	
			35					40					45			
aga	tgg	gag	gca	agg	agc	ttt	atc	gaa	ata	ttt	gga	caa	att	gat	tca	191
Arg	Trp	Glu	Ala	Arg	Ser	Phe	Ile	Glu	Ile	Phe	Gly	Gln	Ile	Asp	Ser	
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gag	ctt	aag	tcg	aat	ttg	agc	aaa	aaa	atg	tta	gag	ttg	gcg	aaa	ttg	239
Glu	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Lys	Met	Leu	Glu	Leu	Ala	Lys	Leu	
	65					70					75					
gac	ttc	aat	att	ctg	caa	tgc	aca	cat	cag	aaa	gaa	ctg	cag	att	atc	287
Asp	Phe	Asn	Ile	Leu	Gln	Cys	Thr	His	Gln	Lys	Glu	Leu	Gln	Ile	Ile	
	80				85				90					95		
tca	agg	tgg	ttc	gca	gac	tca	agt	ata	gca	tcc	ctg	aat	ttc	tat	cgg	335
Ser	Arg	Trp	Phe	Ala	Asp	Ser	Ser	Ile	Ala	Ser	Leu	Asn	Phe	Tyr	Arg	
				100					105					110		
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Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu	
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ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	gct	ata	ctg	431
Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu	
		130					135					140				
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa	479
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln	
	145					150					155					
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	tcg	ttg	gta	527
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val	
160					165			170							175	
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag	575
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys	
				180					185					190		
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp	
			195				200					205				
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Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala	
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Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe	
	225					230				235						
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu	
240					245					250					255	
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggt	gaa	cat	tta	cca	atc	gac	att	815
Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile	
				260				265						270		
ctg	gag	caa	ata	ttc	ttg	ccc	tcc	agg	ttc	cac	cat	ctc	att	gaa	ttg	863
Leu	Glu	Gln	Ile	Phe	Leu	Pro	Ser	Arg	Phe	His	His	Leu	Ile	Glu	Leu	
			275				280						285			
gct	tcc	agg	ctc	gtc	gat	gac	gcg	aga	gat	ttc	cag	gcg	gag	aag	gat	911
Ala	Ser	Arg	Leu	Val	Asp	Asp	Ala	Arg	Asp	Phe	Gln	Ala	Glu	Lys	Asp	
		290					295					300				
cat	ggg	gat	tta	tcg	tgt	att	gag	tgt	tat	tta	aaa	gat	cat	cct	gag	959
His	Gly	Asp	Leu	Ser	Cys	Ile	Glu	Cys	Tyr	Leu	Lys	Asp	His	Pro	Glu	
	305					310					315					
tct	aca	gta	gaa	gat	gct	tta	aat	cat	gtt	aat	ggc	ctc	ctt	ggc	aat	1007
Ser	Thr	Val	Glu	Asp	Ala	Leu	Asn	His	Val	Asn	Gly	Leu	Leu	Gly	Asn	
320					325					330					335	
tgc	ctt	ctg	gaa	atg	aat	tgg	aag	ttc	tta	aag	aag	cag	gac	agt	gtg	1055
Cys	Leu	Leu	Glu	Met	Asn	Trp	Lys	Phe	Leu	Lys	Lys	Gln	Asp	Ser	Val	
				340				345						350		
cca	ctc	tcg	tgt	aag	aag	tac	agc	ttc	cat	gta	ttg	gca	cga	agc	atc	1103
Pro	Leu	Ser	Cys	Lys	Lys	Tyr	Ser	Phe	His	Val	Leu	Ala	Arg	Ser	Ile	

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caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg			1151
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val			
370	375	380	
atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga			1199
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile			
385	390	395	
tagtagatac tagatagtag attagtagct attagtattt atttcatatc aatatttact			1259
aatgctgatg atggttaaag tccattcaga ccaatctttg gtttattgga cttaaataaaa			1319
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Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg			
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Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu			
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Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp			
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Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser			
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Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys			
100	105	110	
Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro			
115	120	125	
Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met			
130	135	140	
Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu			
145	150	155	160
Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu			
165	170	175	
Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr			
180	185	190	

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

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<211> 23
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<220>
<223> Description of Artificial Sequence:
oligonucleotide PCR primer E wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer E wherein the letter n represents
inosine

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ggngaramrr tnatggarga rgc

<210> 22

<211> 24
<212> DNA
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<220>

<223> Description of Artificial Sequence: degenerate
oligonucleotide primer F wherein the letter "n"
represents an inosine residue

<220>

<221> misc_feature

<222> (1)..(24)

<223> PCR primer F wherein the letter n represents
inosine

<400> 22

garytnccary tnhbnmgntg gtgg

24

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer G wherein the letter
"n" represents an inosine residue

<220>

<221> misc_feature

<222> (1)..(21)

<223> PCR primer G wherein the letter n represents
inosine

<400> 23

ccarttnarn ccyttnacrt c

21

<210> 24

<211> 533

<212> DNA

<213> Abies grandis

<400> 24

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cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtcttttg acaggacact 180

gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240

aacatctttc aatccttact cgcataatcc cattgcaacc cattctgaca atggacatcc 300

cctttcctga tcatatcctc aaggaagttg acttcccatc aaagcttaac gacttgatc 360

gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420

aagaagcttc ctctatatca tggtatatga aagacaatcc tggagtatca gaggaagatg 480

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533

<210> 25

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer D was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at position number 4 represents Ile or Tyr or Phe, Xaa at position number 6 represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>

<221> SITE

<222> (1)..(8)

<223> conserved amino acid motif on which sequence of primer D was based

<400> 25

Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer E was based wherein Xaa at position 3 represents Lys or Thr, Xaa at position 4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>

<221> SITE

<222> (1)..(8)

<223> conserved amino acid sequence on which the sequence of primer E was based

<400> 26

Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid sequence on which the sequence of primer F was based wherein Xaa at position 2 represents Phe or Tyr or Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu
or Arg

<220>

<221> SITE

<222> (1)..(7)

<223> conserved amino acid sequence on which the
sequence of primer F was based

<400> 27

Gln Xaa Xaa Xaa Arg Trp Trp
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<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of primer G
was based wherein Xaa at position 6 represents Phe or Leu

<220>

<221> SITE

<222> (1)..(8)

<223> conserved amino acid sequence on which the
sequence of primer G was based

<400> 28

Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: T3 primer
oligonucleotide sequence

<400> 29

aattaaccct cactaaaggg

20

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: T7
oligonucleotide primer sequence

<400> 30

gtaatacgac tcactatagg gc

22

<210> 31
 <211> 2205
 <212> DNA
 <213> Abies grandis

<220>
 <221> CDS
 <222> (57)..(1943)
 <223> Clone AG3.48

<400> 31
 gttatcttga gcttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59
 Met
 1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
 Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
 5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
 Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
 20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
 Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met
 35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
 Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
 50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
 Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
 70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
 Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
 85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
 Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
 100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
 Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
 115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491
 Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu
 130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539
 Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly
 150 155 160

att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587
 Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala
 165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro	Glu		
		180					185					190					
gtt	tta	aaa	gct	ttt	caa	gat	caa	aat	gga	cag	ttt	gta	tgc	tcc	ccc	683	
Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser	Pro		
	195					200					205						
ggt	cag	aca	gag	ggt	gag	atc	aga	agc	ggt	ctt	aac	tta	tat	cgg	gct	731	
Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala		
210					215					220					225		
tcc	ctc	att	gcc	ttc	cct	ggt	gag	aaa	ggt	atg	gaa	gaa	gct	gaa	atc	779	
Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	Ile		
				230					235					240			
ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	cca	gtc	tcc	827	
Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val	Ser		
			245					250					255				
gct	ctt	tca	caa	gag	ata	aag	ttt	ggt	atg	gaa	tat	ggc	tgg	cac	aca	875	
Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His	Thr		
		260					265					270					
aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	ctt	gag	aaa	923	
Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu	Lys		
	275					280					285						
gac	acc	agt	gca	tgg	ctc	aat	aaa	aat	gct	ggg	aag	aag	ctt	tta	gaa	971	
Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Leu	Glu		
290					295				300						305		
ctt	gca	aaa	ttg	gag	ttc	aat	ata	ttt	aac	tcc	tta	caa	caa	aag	gaa	1019	
Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys	Glu		
				310					315					320			
tta	caa	tat	ctt	ttg	aga	tgg	tgg	aaa	gag	tcg	gat	ttg	cct	aaa	ttg	1067	
Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys	Leu		
				325				330					335				
aca	ttt	gct	cgg	cat	cgt	cat	gtg	gaa	ttc	tac	act	ttg	gcc	tct	tgt	1115	
Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser	Cys		
		340					345					350					
att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	ttc	gcc	aaa	1163	
Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala	Lys		
	355					360					365						
atg	tgt	cat	ctt	gtc	aca	ggt	ttg	gac	gat	att	tac	gac	act	ttt	gga	1211	
Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly		
370					375					380				385			
acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	aga	tgg	aat	1259	
Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp	Asn		
				390					395					400			
tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	gtg	tac	atg	1307	
Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr	Met		
				405				410					415				
gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	gag	aag	act	1355	
Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	Glu	Lys	Thr		

420	425	430	
caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat			1403
Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr			
435	440	445	
ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg			1451
Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu			
450	455	460	465
cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat			1499
Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr			
	470	475	480
cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct			1547
Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro			
	485	490	495
gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg			1595
Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu			
	500	505	510
gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc tac aag gcc			1643
Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala			
	515	520	525
gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa			1691
Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys			
530	535	540	545
gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc			1739
Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala			
	550	555	560
atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc			1787
Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser			
	565	570	575
aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca			1835
Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr			
	580	585	590
aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc			1883
Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala			
	595	600	605
aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg			1931
Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met			
610	615	620	625
ctt ttt taa cta taaccatatt cataataata agctcataat gctaaattat			1983
Leu Phe			
ttgccttatg acatagttta tgtatgtact tgtgtgaatt caatcatatc gtgtgggtat			2043
gattaaaaag ctagagctta ctaggttagt aacatggtga taaaagttat aaaatgtgag			2103
ttatagagat acccatgttg aataatgaat tacaaaaaga gaaatttatg tagaataaga			2163
ttggaagctt ttcaattggt ttaaaaaaaaa aaaaaaaaaa aa			2205

<210> 32
 <211> 627
 <212> PRT
 <213> Abies grandis

<400> 32
 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
 1 5 10 15
 Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
 20 25 30
 Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
 35 40 45
 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
 50 55 60
 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
 65 70 75 80
 Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
 85 90 95
 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
 100 105 110
 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
 115 120 125
 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
 130 135 140
 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
 145 150 155 160
 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
 165 170 175
 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
 180 185 190
 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
 195 200 205
 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
 210 215 220
 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
 225 230 235 240
 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
 245 250 255
 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
 260 265 270
 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
 275 280 285

Lys	Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Leu			
290						295					300							
Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys			
305					310					315					320			
Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys			
				325					330					335				
Leu	Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser			
			340					345					350					
Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala			
		355					360					365						
Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe			
	370					375					380							
Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp			
385					390					395					400			
Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr			
				405					410					415				
Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	Glu	Lys			
			420					425					430					
Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	Glu	Ala			
		435					440					445						
Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	Gly	Tyr			
	450					455					460							
Leu	Pro	Thr	Phe	Glu	Glu	Tyr	His	Glu	Asn	Gly	Lys	Val	Ser	Ser	Ala			
465					470					475					480			
Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	Trp	Leu			
				485					490					495				
Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	Asn	Asp			
			500					505					510					
Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys			
		515					520					525						
Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	Tyr	Met			
	530					535					540							
Lys	Asp	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn			
545					550					555					560			
Ala	Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg			
				565					570					575				
Ser	Asn	Asp	Asn	Ile	Pro	Met	Leu	Ala	Lys	Lys	His	Ala	Phe	Asp	Ile			
			580					585					590					
Thr	Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	Ser	Val			
		595					600					605						
Ala	Asn	Lys	Glu	Thr	Lys	Lys	Leu	Val	Met	Glu	Thr	Leu	Leu	Glu	Ser			

610

615

620

Met Leu Phe
625

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 BamHI

<400> 33
caaagggatc cagaatggct ctgg

24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 Not I

<400> 34
agtaagcggc cgctttttaa tcataccac

30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c

21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 SmaI

<400> 36
catagccccg ggcatagatt tgagctg

27

<210> 37
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 NdeI

<400> 37

ggcaggaaca tatggctctc ctttctatcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2-8

<400> 40

gttggatctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-11

<400> 42
cgtaatggaa agctctggcg 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 7-1

<400> 43
ccttacacgc ctttggatgg 20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide sequence 7-3

<400> 44
tctgttgatc caggatggtc 20

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif common to all prenyl transferases wherein Xaa at
position
3 and 4 represents any amino acid

<400> 45
Asp Asp Xaa Xaa Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents
Leu or Ile or Val

<400> 46

His Ser Asn Xaa Trp Asp Asp Asp
1 5

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47

Ala Leu Asp Tyr Val Tyr
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49

Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention, wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 50
Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 51
Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to the monoterpene
synthase clones of the present invention, wherein Xaa at position 1
represents Val or Ile or Leu

<400> 52
Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53

Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54

atgatgatg

9

<210> 55

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55

tactactac

9

<210> 56

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56

nacnacnac

9

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide corresponding to amino acid sequence set forth in SEQ ID NO:46

<220>
<221> misc_feature
<222> (1)..(24)
<223> Oligonucleotide that corresponds to the conserved
amino acid sequence set forth in SEQ ID NO:46

<400> 57
gtgtcgttgg agaccctgct gctg

24

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:47

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:47

<400> 58
cgggagctga tgcagatg

18

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:48

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:48

<400> 59
ctcgagcggg tgcgagctcaa g

21

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:49

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:49

<400> 60
gccaccacct tcctctcg

18

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<400> 61
gaggagctgc tgtacatgct g

21

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:51

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide corresponding to conserved amino
acid sequence set forth in SEQ ID NO:51

<400> 62
gaggagctgc tggagatgct g

21

<210> 63
<211> 293
<212> DNA
<213> Abies grandis

<400> 63
cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caactatatt 60
cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

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Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser Ser His Glu Ile Lys
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Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys
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tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr
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Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val	
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Thr Lys Met Ser His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Val	
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Phe	Pro	Asp	His	Ile	Leu	Lys	Glu	Val	Asp	Phe	Pro	Ser	Lys	Leu	Asn		
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Asp	Leu	Ile	Cys	Ile	Ile	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr		
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Lys	Ala	Asp	Arg	Ala	Arg	Gly	Glu	Glu	Ala	Ser	Ser	Ile	Ser	Cys	Tyr		
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Met	Lys	Asp	Asn	Pro	Gly	Leu	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile		
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Pro	Val	Pro	Leu														
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Thr	Ser	Val	Ala	Ser	Thr	Asp	Ser	Val	Gln	Arg	Arg	Val	Gly	Asn	Tyr
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His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ile	Ser	Thr
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Pro	Tyr	Gly	Ala	Pro	Asp	Tyr	Arg	Glu	Arg	Ala	Asp	Arg	Leu	Ile	Gly
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Glu	Val	Lys	Asp	Ile	Met	Phe	Asn	Phe	Lys	Ser	Leu	Glu	Asp	Gly	Gly
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Gly	Ile	Asp	Arg	His	Phe	Lys	Lys	Glu	Ile	Lys	Thr	Ala	Leu	Asp	Tyr
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Val	Asn	Ser	Tyr	Trp	Asn	Glu	Lys	Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser
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Val	Val	Thr	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg
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Leu	His	Gly	Tyr	Thr	Val	Ser	Ser	Asp	Val	Leu	Asn	Val	Phe	Lys	Asp
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Arg	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Ala	Ser	Ser	Ile	Leu	Ser	Leu	Glu
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Phe	His	Ser	Leu	Gln	Glu	Arg	Glu	Leu	Lys	His	Val	Ser	Arg	Trp	Trp	305	310	315	320
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Glu	Tyr	Met	Lys	Gly	Val	Tyr	Met	Met	Val	Tyr	His	Thr	Val	Asn	Glu		405	410	415
Met	Ala	Arg	Val	Ala	Glu	Lys	Ala	Gln	Gly	Arg	Asp	Thr	Leu	Asn	Tyr		420	425	430
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Phe	Pro	Ser	Lys	Leu	Asn	Asp	Leu	Ile	Cys	Ile	Ile	Leu	Arg	Leu	Arg		500	505	510
Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly	Glu	Glu	Ala		515	520	525
Ser	Ser	Ile	Ser	Cys	Tyr	Met	Lys	Asp	Asn	Pro	Gly	Leu	Thr	Glu	Glu	530	535	540	
Asp	Ala	Leu	Asn	His	Ile	Asn	Phe	Met	Ile	Arg	Asp	Ala	Ile	Arg	Glu	545	550	555	560
Leu	Asn	Trp	Glu	Leu	Leu	Lys	Pro	Asp	Asn	Ser	Val	Pro	Ile	Thr	Ser		565	570	575
Lys	Lys	His	Ala	Phe	Asp	Ile	Ser	Arg	Val	Trp	His	His	Gly	Tyr	Arg		580	585	590
Tyr	Arg	Asp	Gly	Tyr	Ser	Phe	Ala	Asn	Val	Glu	Thr	Lys	Ser	Leu	Val		595	600	605
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ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val
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tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro
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Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met
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Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn
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Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly
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att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val
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tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val
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ttt cct gat gtc aac tcg act gcc tcg ggg ttt cga act ctt cgc cta 582
Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu
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Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe	
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Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro	
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Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn	
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Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn	
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Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe	
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Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile
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Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu
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Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu
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Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly
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Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val
 115 120 125

Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
 130 135 140

Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile
 145 150 155 160

Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
 165 170 175

Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
 180 185 190

Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
 195 200 205

Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
 210 215 220

Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe
 225 230 235 240

Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser
 245 250 255

Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn
 260 265 270

Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro
 275 280 285

Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu
 290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
 305 310 315 320
 Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly
 325 330 335
 Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr
 340 345 350
 Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu
 355 360 365
 Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
 370 375 380
 Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val
 385 390 395 400
 Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys
 405 410 415
 Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu
 420 425 430
 Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala
 435 440 445
 Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala
 450 455 460
 Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val
 465 470 475 480
 Ser Ser Gly His Arg Ala Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp
 485 490 495
 Val Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg
 500 505 510
 Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg
 515 520 525
 Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser
 530 535 540
 Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn
 545 550 555 560
 His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu
 565 570 575
 Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala
 580 585 590
 Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly
 595 600 605
 Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val
 610 615 620

Leu Glu Pro Val Pro Leu
625 630

<210> 68
<211> 2429
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (35)..(1945)

<400> 68
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Met Ala Leu Leu Ser Ile Val
1 5

tct ttg cag gtt ccc aaa tcc tgc ggg ctg aaa tcg ttg atc agt tcc 103
Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser
10 15 20

agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc 151
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu
25 30 35

aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc 199
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr
40 45 50 55

act gta tcc cat cgt gat gat aat ggt ggt ggt gta ctg caa aga cgc 247
Thr Val Ser His Arg Asp Asp Asn Gly Gly Gly Val Leu Gln Arg Arg
60 65 70

ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca 295
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser
75 80 85

ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca 343
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr
90 95 100

gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga 391
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg
105 110 115

gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg 439
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val
120 125 130 135

gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata 487
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile
140 145 150

aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc 535
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly
155 160 165

att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct 583
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala
170 175 180

ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat	631
Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp	
185 190 195	
gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca	679
Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala	
200 205 210 215	
atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg	727
Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg	
220 225 230	
gct tcc ctg gtc gcc ttt ccg ggg gag aaa gtt atg gaa gag gct gaa	775
Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu	
235 240 245	
atc ttc tcg gca tct tat ttg aaa gaa gtc tta caa aag att cca gtc	823
Ile Phe Ser Ala Ser Tyr Leu Lys Glu Val Leu Gln Lys Ile Pro Val	
250 255 260	
tcc agt ttt tca cga gag ata gaa tac gtt ttg gaa tat ggt tgg cac	871
Ser Ser Phe Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Gly Trp His	
265 270 275	
aca aat ttg cca aga ttg gaa gca aga aat tat atc gac gtc tac ggg	919
Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Tyr Gly	
280 285 290 295	
cag gac agc tat gaa agt tca aac gag atg cca tat gtg aat acg cag	967
Gln Asp Ser Tyr Glu Ser Ser Asn Glu Met Pro Tyr Val Asn Thr Gln	
300 305 310	
aag ctt tta aaa ctt gca aaa ttg gag ttt aat atc ttt cac tct ttg	1015
Lys Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu	
315 320 325	
caa cag aaa gag ttg caa tat atc tct aga tgg tgg aaa gat tcg tgt	1063
Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys	
330 335 340	
tca tct cat ctg act ttt act cga cac cgt cac gtg gaa tac tac aca	1111
Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr	
345 350 355	
atg gca tct tgc att tct atg gag ccg aaa cac tcc gct ttc aga ttg	1159
Met Ala Ser Cys Ile Ser Met Glu Pro Lys His Ser Ala Phe Arg Leu	
360 365 370 375	
ggg ttt gtc aaa aca tgt cat ctt cta aca gtt ctg gat gat atg tat	1207
Gly Phe Val Lys Thr Cys His Leu Leu Thr Val Leu Asp Asp Met Tyr	
380 385 390	
gac act ttt gga aca ctg gac gaa ctc caa ctt ttt acg act gcc ttt	1255
Asp Thr Phe Gly Thr Leu Asp Glu Leu Gln Leu Phe Thr Thr Ala Phe	
395 400 405	
aag aga tgg gat ttg tca gag aca aag tgt ctt cca gaa tat atg aaa	1303
Lys Arg Trp Asp Leu Ser Glu Thr Lys Cys Leu Pro Glu Tyr Met Lys	
410 415 420	

gca gtg tac atg gac ttg tat caa tgt ctt aat gaa ttg gcg caa gag	1351
Ala Val Tyr Met Asp Leu Tyr Gln Cys Leu Asn Glu Leu Ala Gln Glu	
425 430 435	
gct gag aag act caa ggc aga gat acg ctc aac tat att cgc aat gct	1399
Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ile Arg Asn Ala	
440 445 450 455	
tat gag tct cat ttt gat tcg ttt atg cac gaa gca aaa tgg atc tca	1447
Tyr Glu Ser His Phe Asp Ser Phe Met His Glu Ala Lys Trp Ile Ser	
460 465 470	
agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt	1495
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val	
475 480 485	
agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat	1543
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp	
490 495 500	
gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg	1591
Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg	
505 510 515	
ttc aat gac ttg gct tcg tcc ctc ctt cgg cta cgt ggt gac acg cgc	1639
Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg	
520 525 530 535	
tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg	1687
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser	
540 545 550	
tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat	1735
Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn	
555 560 565	
cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag	1783
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu	
570 575 580	
ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct	1831
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala	
585 590 595	
ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt	1879
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly	
600 605 610 615	
tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt	1927
Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val	
620 625 630	
ctt gaa cct gtg gca ttg taataata tcaaccgcat caaatgcac	1975
Leu Glu Pro Val Ala Leu	
635	
ggagtttgta atttaatgca cttctcttat aatacacttc tcttttagacc tgtagtgaag	2035
ccgatgcacc attacagtgt atatgggagc cagtctagtc tcaaaaagtt tgtaaagtgt	2095
attctatgat atactcttta gaccaaagc tagatgccca tgaaaagcaa gtgtttttaga	2155

attgcttctg gatttgctta aattttctcc atgattcttt agaaatgttg catccccaaa 2215
cttcactgcc atataagata acgggagtga caaggatttt aaagaggatt tttttttatg 2275
tcccgcata caaggtttgt cgatttacag ttgttttcaa gactgaagta ggatttccac 2335
cctccattaa tcctcttctc gatgttatag tttcacttga gcttgtgatg gaagtcaatt 2395
cctagatatt tataagaaaa aaaaaaaaaa aaaa 2429

<210> 69
<211> 637
<212> PRT
<213> *Abies grandis*

<400> 69
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15
Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30
Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45
Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60
Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80
Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95
Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110
Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125
Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140
Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160
Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175
Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190
Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
195 200 205
Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220
Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu

225						230						235						240
Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Glu			
				245					250					255				
Val	Leu	Gln	Lys	Ile	Pro	Val	Ser	Ser	Phe	Ser	Arg	Glu	Ile	Glu	Tyr			
				260					265					270				
Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg			
				275					280					285				
Asn	Tyr	Ile	Asp	Val	Tyr	Gly	Gln	Asp	Ser	Tyr	Glu	Ser	Ser	Asn	Glu			
				290					295					300				
Met	Pro	Tyr	Val	Asn	Thr	Gln	Lys	Leu	Leu	Lys	Leu	Ala	Lys	Leu	Glu			
				305					310					315				
Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Gln	Lys	Glu	Leu	Gln	Tyr	Ile	Ser			
				325					330					335				
Arg	Trp	Trp	Lys	Asp	Ser	Cys	Ser	Ser	His	Leu	Thr	Phe	Thr	Arg	His			
				340					345					350				
Arg	His	Val	Glu	Tyr	Tyr	Thr	Met	Ala	Ser	Cys	Ile	Ser	Met	Glu	Pro			
				355					360					365				
Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Val	Lys	Thr	Cys	His	Leu	Leu			
				370					375					380				
Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	Thr	Phe	Gly	Thr	Leu	Asp	Glu	Leu			
				385					390					395				
Gln	Leu	Phe	Thr	Thr	Ala	Phe	Lys	Arg	Trp	Asp	Leu	Ser	Glu	Thr	Lys			
				405					410					415				
Cys	Leu	Pro	Glu	Tyr	Met	Lys	Ala	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys			
				420					425					430				
Leu	Asn	Glu	Leu	Ala	Gln	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Thr			
				435					440					445				
Leu	Asn	Tyr	Ile	Arg	Asn	Ala	Tyr	Glu	Ser	His	Phe	Asp	Ser	Phe	Met			
				450					455					460				
His	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Gly	Tyr	Leu	Pro	Thr	Phe	Glu	Glu			
				465					470					475				
Tyr	Leu	Lys	Asn	Gly	Lys	Val	Ser	Ser	Gly	Ser	Arg	Thr	Ala	Thr	Leu			
				485					490					495				
Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asn	Tyr	Ile	Leu	Gln			
				500					505					510				
Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Asp	Leu	Ala	Ser	Ser	Leu	Leu			
				515					520					525				
Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly			
				530					535					540				
Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	Pro	Gly	Ser			
				545					550					555				

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70
<211> 696
<212> DNA
<213> *Abies grandis*

<400> 70
gcatttaaga gatgggatcc gtctgccaca gatttgcttc cagagtatat gaaaggggtg 60
tacatggtgg ttacgaaac cgtaaataaa attgctcgag aggcagacaa gtctcaaggc 120
cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgatgc gtatatgaaa 180
gaagctgagt ggatctccag tgggttatctg ccaacgtttg aggagtacat ggagaccagc 240
aaagttagtt ttggttatcg catattcgca ttgcaacca tcctcactat ggatgttccc 300
cttactcacc acatcctgca ggaaatagac tttccattga ggtttaatga cttaatatgt 360
tccatccttc gacttaaaaa tgacactcgc tgctacaagg cggacagggc ccgtggagaa 420
gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480
atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattg ggagcttctc 540
cgacaggacg gcaccgctca tattgcttgc aagaaacacg cttttgacat cctcaaaggt 600
tcccttcacg gctacaaata ccgagatggg ttcagcgttg ccaacaagga aaccaagaat 660
tggttgagga gaacagtcct tgagtctgtg cctttg 696

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse RACE primer 10-2

<400> 71
acgaagcttc ttctccacgg

20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse RACE primer 10-4

<400> 72
ggatcccatc tcttaactgc

20

<210> 73
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(27)
<223> PCR primer AP1

<400> 73
ccatccta acgactcact atagggc

27

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer AP2

<400> 74
actcactata gggctcgagc ggc

23

<210> 75
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9F

<400> 75
atggctcttg tttctatctt gccc

24

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9R

<400> 76
ttacaaaggc acagactcaa ggac

24

<210> 77
<211> 1890
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (1)..(1890)

<400> 77
atg gct ctt gtt tct atc ttg ccc ttg tct tcc aaa tcg gtc ctg cac 48
Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

Arg	Arg	Ile	Val	Glu	Phe	His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Phe	Ile		
65					70					75					80		
caa	tct	cta	tca	acg	cct	tat	ggg	gca	cct	tca	tac	cgt	gaa	cgt	gct		288
Gln	Ser	Leu	Ser	Thr	Pro	Tyr	Gly	Ala	Pro	Ser	Tyr	Arg	Glu	Arg	Ala		
				85					90					95			
gat	aga	ctt	att	gtg	gaa	gta	aag	ggg	ata	ttc	act	tca	att	tca	gcg		336
Asp	Arg	Leu	Ile	Val	Glu	Val	Lys	Gly	Ile	Phe	Thr	Ser	Ile	Ser	Ala		
			100					105					110				
gaa	gat	gga	gaa	cta	atc	act	ccc	ctc	aat	gat	ctc	att	caa	cgc	ctt		384
Glu	Asp	Gly	Glu	Leu	Ile	Thr	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu		
		115					120					125					
tta	atg	gtc	gat	aac	gtt	gaa	cgt	tta	ggg	att	gat	aga	cat	ttc	aaa		432
Leu	Met	Val	Asp	Asn	Val	Glu	Arg	Leu	Gly	Ile	Asp	Arg	His	Phe	Lys		
	130					135					140						
aat	gag	ata	aaa	gca	gca	cta	gac	tat	gtt	tac	agt	tat	tgg	aac	gaa		480
Asn	Glu	Ile	Lys	Ala	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Asn	Glu		
145					150					155					160		
aaa	ggc	att	ggc	agt	gga	agt	gat	agt	ggg	gtt	gct	gat	ctc	aac	tca		528
Lys	Gly	Ile	Gly	Ser	Gly	Ser	Asp	Ser	Gly	Val	Ala	Asp	Leu	Asn	Ser		
				165					170					175			
act	gcc	ctg	ggg	ttt	cga	att	ctt	cga	cta	cac	gga	tac	agt	gtt	tct		576
Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser		
			180					185					190				
tca	gat	gtg	ttg	gaa	cac	ttc	aaa	gag	gag	aag	gag	aag	ggg	cag	ttt		624
Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe		
		195					200					205					
gta	tgt	tcg	gcc	atc	caa	aca	gag	gaa	gag	ata	aaa	agc	gtt	ctg	aat		672
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn		
	210					215					220						
tta	ttt	cgg	gcc	tcc	ctc	att	gcc	ttt	cct	ggg	gag	aaa	gtt	atg	gaa		720
Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu		
225					230					235					240		
gag	gct	gaa	atc	ttc	tct	aaa	ata	tat	tta	aaa	gaa	gcc	tta	caa	aat		768
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn		
				245					250				255				
att	gct	gtc	tcc	agt	ctt	tca	cga	gag	ata	gag	tac	gtt	ctg	gag	gat		816
Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp		
			260					265					270				
ggg	tgg	caa	aca	aat	atg	cca	aga	ttg	gaa	aca	agg	aac	tac	atc	gat		864
Gly	Trp	Gln	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	Asn	Tyr	Ile	Asp		
		275					280					285					
gta	ttg	gga	gag	aac	gat	cgt	gat	gag	acg	tta	tat	atg	aac	atg	gag		912
Val	Leu	Gly	Glu	Asn	Asp	Arg	Asp	Glu	Thr	Leu	Tyr	Met	Asn	Met	Glu		
	290					295					300						
aaa	ctt	tta	gaa	att	gca	aaa	ttg	gag	ttc	aat	att	ttt	cac	tcc	tta		960
Lys	Leu	Leu	Glu	Ile	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu		

305					310					315					320	
caa	cag	aga	gag	cta	aaa	gac	ctc	tcc	aga	tgg	tgg	aaa	gat	tcg	ggt	1008
Gln	Gln	Arg	Glu	Leu	Lys	Asp	Leu	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Gly	
				325					330					335		
ttc	tct	cac	ctg	aca	ttt	tct	cgg	cat	cgt	cat	gtg	gaa	ttc	tac	gct	1056
Phe	Ser	His	Leu	Thr	Phe	Ser	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Ala	
			340					345					350			
ctg	gca	tct	tgc	att	gaa	act	gat	cgc	aaa	cat	tcc	gga	ttc	aga	ctc	1104
Leu	Ala	Ser	Cys	Ile	Glu	Thr	Asp	Arg	Lys	His	Ser	Gly	Phe	Arg	Leu	
		355					360					365				
ggc	ttt	gcc	aaa	atg	tgt	cat	ctt	atc	acg	gtt	ttg	gac	gat	ata	tac	1152
Gly	Phe	Ala	Lys	Met	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Ile	Tyr	
	370					375					380					
gac	acc	ttt	gga	aca	atg	gag	gag	ctg	gaa	ctc	ttc	act	gca	gca	ttt	1200
Asp	Thr	Phe	Gly	Thr	Met	Glu	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Ala	Phe	
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aag	aga	tgg	gat	ccg	tct	gcc	aca	gat	ttg	ctt	cca	gag	tat	atg	aaa	1248
Lys	Arg	Trp	Asp	Pro	Ser	Ala	Thr	Asp	Leu	Leu	Pro	Glu	Tyr	Met	Lys	
				405					410					415		
ggg	ttg	tac	atg	gtg	gtt	tac	gaa	acc	gta	aat	gaa	att	gct	cga	gag	1296
Gly	Leu	Tyr	Met	Val	Val	Tyr	Glu	Thr	Val	Asn	Glu	Ile	Ala	Arg	Glu	
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gca	gac	aag	tct	caa	ggc	cga	gag	acg	ctc	aac	gat	gct	cga	cga	gct	1344
Ala	Asp	Lys	Ser	Gln	Gly	Arg	Glu	Thr	Leu	Asn	Asp	Ala	Arg	Arg	Ala	
		435					440					445				
tgg	gag	gcc	tat	ctt	gat	tcg	tat	atg	aaa	gaa	gct	gag	tgg	atc	tcc	1392
Trp	Glu	Ala	Tyr	Leu	Asp	Ser	Tyr	Met	Lys	Glu	Ala	Glu	Trp	Ile	Ser	
	450					455					460					
agt	ggt	tat	ctg	cca	acg	ttt	gag	gag	tac	atg	gag	acc	agc	aaa	gtt	1440
Ser	Gly	Tyr	Leu	Pro	Thr	Phe	Glu	Glu	Tyr	Met	Glu	Thr	Ser	Lys	Val	
	465				470				475						480	
agt	ttt	ggt	tat	cgc	ata	ttc	gca	ttg	caa	ccc	atc	ctc	act	atg	gat	1488
Ser	Phe	Gly	Tyr	Arg	Ile	Phe	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp	
				485					490					495		
gtt	ccc	ctt	act	cac	cac	atc	ctg	cag	gaa	ata	gac	ttt	cca	ttg	agg	1536
Val	Pro	Leu	Thr	His	His	Ile	Leu	Gln	Glu	Ile	Asp	Phe	Pro	Leu	Arg	
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ttt	aat	gac	tta	ata	tgt	tcc	atc	ctt	cga	ctt	aaa	aat	gac	act	cgc	1584
Phe	Asn	Asp	Leu	Ile	Cys	Ser	Ile	Leu	Arg	Leu	Lys	Asn	Asp	Thr	Arg	
		515					520					525				
tgc	tac	aag	gcg	gac	agg	gcc	cgt	gga	gaa	gaa	gct	tcg	tgt	ata	tcg	1632
Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	
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tgt	tat	atg	aaa	gag	aat	cct	gga	tca	aca	gag	gaa	gat	gct	atc	aat	1680
Cys	Tyr	Met	Lys	Glu	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Ile	Asn	
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cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag	1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu	
565 570 575	
ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct	1776
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala	
580 585 590	
ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg	1824
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly	
595 600 605	
ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc	1872
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val	
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ctt gag tct gtg cct ttg	1890
Leu Glu Ser Val Pro Leu	
625 630	

<210> 78
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 <212> PRT
 <213> Abies grandis

<400> 78

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Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser	
35 40 45	
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln	
50 55 60	
Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile	
65 70 75 80	
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala	
85 90 95	
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala	
100 105 110	
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu	
115 120 125	
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys	
130 135 140	
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu	
145 150 155 160	
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser	
165 170 175	

Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser			
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Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe			
		195					200					205						
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn			
	210					215					220							
Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu			
225					230					235					240			
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn			
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Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp			
			260					265					270					
Gly	Trp	Gln	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	Asn	Tyr	Ile	Asp			
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Val	Leu	Gly	Glu	Asn	Asp	Arg	Asp	Glu	Thr	Leu	Tyr	Met	Asn	Met	Glu			
	290					295					300							
Lys	Leu	Leu	Glu	Ile	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu			
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Gln	Gln	Arg	Glu	Leu	Lys	Asp	Leu	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Gly			
				325					330					335				
Phe	Ser	His	Leu	Thr	Phe	Ser	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Ala			
			340					345					350					
Leu	Ala	Ser	Cys	Ile	Glu	Thr	Asp	Arg	Lys	His	Ser	Gly	Phe	Arg	Leu			
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Gly	Phe	Ala	Lys	Met	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Ile	Tyr			
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Lys	Arg	Trp	Asp	Pro	Ser	Ala	Thr	Asp	Leu	Leu	Pro	Glu	Tyr	Met	Lys			
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Gly	Leu	Tyr	Met	Val	Val	Tyr	Glu	Thr	Val	Asn	Glu	Ile	Ala	Arg	Glu			
			420					425					430					
Ala	Asp	Lys	Ser	Gln	Gly	Arg	Glu	Thr	Leu	Asn	Asp	Ala	Arg	Arg	Ala			
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Trp	Glu	Ala	Tyr	Leu	Asp	Ser	Tyr	Met	Lys	Glu	Ala	Glu	Trp	Ile	Ser			
	450					455					460							
Ser	Gly	Tyr	Leu	Pro	Thr	Phe	Glu	Glu	Tyr	Met	Glu	Thr	Ser	Lys	Val			
465					470					475					480			
Ser	Phe	Gly	Tyr	Arg	Ile	Phe	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp			
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Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser		
530	535	540
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn		
545	550	555
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu		
565	570	575
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala		
580	585	590
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly		
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 <223> Mutagenesis primer 6eBamHIF

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<400> 81
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<210> 82
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<400> 82
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<210> 83
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<223> Mutagenesis primer 732eNdeIF

<400> 83
cgagatgccca tacgtgaata cgcag

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<210> 84
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<400> 84
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25

<210> 85
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<400> 85
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30

<210> 86
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<400> 86
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34

<210> 87
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29

<210> 88

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<213> Artificial Sequence

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<400> 88

taagcgagca catatggctc tggtttcttc

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<210> 89

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<210> 90

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<400> 90

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<210> 91

<211> 34
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<400> 91
ggtcgactct agaggatcca ctagtgatat ggat

34

<210> 92
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<400> 92
gaacatatgg ctctcctttc tatcgta

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<210> 93
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<400> 93
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<210> 94
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<400> 94
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34

<210> 95
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<400> 95
caaagggagc acatatggct ctgg

24

<210> 96
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<400> 96
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<210> 97
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<400> 97

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28

<210> 98
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<400> 98
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<210> 99
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<400> 99
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<210> 100
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<400> 100
cgtttgggaa tccatagaca tttc

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<210> 101
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<400> 101
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24

<210> 102
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<220>
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<223> PCR primer 3e2BamHIF

<400> 102
gaagagatgg gacccgtcct cgatag

26

<210> 103
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<400> 103
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<220>
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<222> (1)..(25)
<223> Mutagenesis primer 3e1NdeIF

<400> 104
gaacacgaag tcctatgtga agagc

25

<210> 105
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<220>
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<222> (1)..(25)
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<400> 105
gctcttcaca taggacttcg tgttc

25

<210> 106
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<212> DNA
<213> Artificial Sequence

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<220>
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<222> (1)..(25)
<223> Mutagenesis primer 3e3NdeIF

<400> 106
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25

<210> 107
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oligonucleotide

<220>
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<222> (1)..(25)
<223> Mutagenesis primer 3e2NdeIR

<400> 107
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25